

JUL 08 2002

TECH CENTER 1600/2900



1645

RAW SEQUENCE LISTING

DATE: 06/10/2002

PATENT APPLICATION: US/08/325,278A

TIME: 16:22:34

Input Set : A:\402.app

Output Set: N:\CRF3\06102002\H325278A.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

C--> 6 (i) APPLICANT: Bjorck, Lars
7 Sjobring, Ulf
9 (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
11 (iii) NUMBER OF SEQUENCES: 15
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Seed IP Law Group
15 (B) STREET: 701 Fifth Avenue Suite 6300
16 (C) CITY: Seattle
17 (D) STATE: Washington
18 (E) COUNTRY: USA
19 (F) ZIP: 98104-7092
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/08/325,278A
C--> 29 (B) FILING DATE: 26-Oct-1994
30 (C) CLASSIFICATION:
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Potter, Jane E. R.
34 (B) REGISTRATION NUMBER: 33,332
35 (C) REFERENCE/DOCKET NUMBER: 100084.402
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (206) 622-4900
39 (B) TELEFAX: (206) 682-6031
42 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 305 amino acids
46 (B) TYPE: amino acid
47 (C) STRANDEDNESS: unknown
48 (D) TOPOLOGY: unknown
50 (ii) MOLECULE TYPE: protein
52 (iii) HYPOTHETICAL: NO
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
62 1 5 10 15
64 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser

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65          20          25          30
67  Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
68          35          40          45
70  Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
71          50          55          60
73  Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
74          65          70          75          80
76  Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
77          85          90          95
79  Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
80          100          105          110
82  Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
83          115          120          125
85  Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
86          130          135          140
88  Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
89          145          150          155          160
91  Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
92          165          170          175
94  Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
95          180          185          190
97  Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
98          195          200          205
100  Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
101          210          215          220
103  Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
104          225          230          235          240
106  Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
107          245          250          255
109  Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
110          260          265          270
112  Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
113          275          280          285
115  Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
116          290          295          300
118  Glu
119  305

```

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 921 base pairs

125 (B) TYPE: nucleic acid

126 (C) STRANDEDNESS: double

127 (D) TOPOLOGY: unknown

129 (ii) MOLECULE TYPE: DNA (genomic)

131 (iii) HYPOTHETICAL: NO

133 (vi) ORIGINAL SOURCE:

134 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

140 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA

60

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142 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACCTGCAGA ATTCAAAGGA 120
144 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT 180
146 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA 240
148 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT 300
150 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA 360
152 GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA 420
154 GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA 480
156 AAAGAAGAAG TTACTATTAA AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA 540
158 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA 600
160 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT 660
162 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA 720
164 AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA 780
166 GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA 840
168 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC 900
170 GAAAAACCAG AAGAATAATA A 921

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172 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 434 amino acids

176 (B) TYPE: amino acid

177 (C) STRANDEDNESS: unknown

178 (D) TOPOLOGY: unknown

180 (ii) MOLECULE TYPE: protein

182 (iii) HYPOTHETICAL: NO

184 (vi) ORIGINAL SOURCE:

185 (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

191 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
192 1 5 10 15
194 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
195 20 25 30
197 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
198 35 40 45
200 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
201 50 55 60
203 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
204 65 70 75 80
206 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
207 85 90 95
209 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
210 100 105 110
212 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
213 115 120 125
215 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
216 130 135 140
218 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
219 145 150 155 160
221 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
222 165 170 175
224 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu

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225          180          185          190
227    Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
228          195          200          205
230    Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
231          210          215          220
233    Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
234    225          230          235          240
236    Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
237          245          250          255
239    Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
240          260          265          270
242    Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
243          275          280          285
245    Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
246    290          295          300
248    Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
249    305          310          315          320
251    Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
252          325          330          335
254    Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
255          340          345          350
257    Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
258          355          360          365
260    Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
261          370          375          380
263    Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
264    385          390          395          400
266    Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
267          405          410          415
269    Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
270          420          425          430
272    Glu Met
275 (2) INFORMATION FOR SEQ ID NO: 4:
277   (i) SEQUENCE CHARACTERISTICS:
278       (A) LENGTH: 1308 base pairs
279       (B) TYPE: nucleic acid
280       (C) STRANDEDNESS: double
281       (D) TOPOLOGY: unknown
283   (ii) MOLECULE TYPE: DNA (genomic)
285   (iii) HYPOTHETICAL: NO
287   (vi) ORIGINAL SOURCE:
288       (A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055
292   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
294 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA      60
296 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAAGTGCAGA ATTCAAAGGA      120
298 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT      180
300 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA      240
302 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT      300
304 GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA      360

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306 GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA      420
308 GATAAAGGTT ATACTTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA      480
310 AAAGAAGAAG TTACTATTAA AGCAAACCTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA      540
312 GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA      600
314 GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT      660
316 AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA      720
318 AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA      780
320 GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA      840
322 GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC      900
324 GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA      960
326 GGCGAAACAA CTACTGAAGC TGTTGATGCT GCTACTGCAG AAAAAGTCTT CAAACAATAC     1020
328 GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTTACA     1080
330 GTTACTGAAA AACCAGAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACCTAC     1140
332 AAACCTGTGA TTAATGGTAA AACATTGAAA GGCGAAACAA CTACTAAAGC AGTAGACGCA     1200
334 GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTGTTG     1260
336 ACTTATGATG ATGCGACTAA GACCTTTACG GTAAC TGAAATAA      1308

338 (2) INFORMATION FOR SEQ ID NO: 5:
340     (i) SEQUENCE CHARACTERISTICS:
341         (A) LENGTH: 1332 base pairs
342         (B) TYPE: nucleic acid
343         (C) STRANDEDNESS: double
344         (D) TOPOLOGY: unknown
346     (ii) MOLECULE TYPE: DNA (genomic)
348     (iii) HYPOTHETICAL: NO
351     (ix) FEATURE:
352         (A) NAME/KEY: CDS
353         (B) LOCATION: 1..1329
356     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
358 AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC      48
359 Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn
360 1 5 10 15
362 AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA      96
363 Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu
364 20 25 30
366 AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG      144
367 Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys
368 35 40 45
370 AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT      192
371 Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg
372 50 55 60
374 AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA      240
375 Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu
376 65 70 75 80
378 GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA      288
379 Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu
380 85 90 95
382 GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG      336
383 Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg
384 100 105 110

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VERIFICATION SUMMARY

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DATE: 06/10/2002

TIME: 16:22:35

Input Set : A:\402.app

Output Set: N:\CRF3\06102002\H325278A.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]